

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN THE APPLICATION OF:
E. I. DUPONT DE NEMOURS AND COMPANY CASE NO.: BB1252 US NA1
APPLICATION NO.: UNKNOWN GROUP ART UNIT: UNKNOWN
FILED: CONCURRENTLY HEREWITH EXAMINER: UNKNOWN
FOR: **DISEASE RESISTANCE FACTORS**

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

DECLARATION IN ACCORDANCE WITH 37 CFR 1.821

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(e) and (e), respectively are the same.

Respectfully submitted,


KENING LI
ATTORNEY FOR APPLICANTS
REGISTRATION NO. 44,872
TELEPHONE: 302-992-3749
FACSIMILE: 302-892-1026

Dated: 04 May 2001

SEQUENCE LISTING

111 S. L. Gilbert & Company
112 Berlin, Maria
Faldo, Karl
Fardis, Emilio G.
Fang, Yiwen
Fan, Feng
Heffard, Elmer
Hsu, Zhan-Bin
Hwang, Gou-Han
Izumi, Juan
Pittman, Amy M.

120 Disease Resistance Factors

130 BB1252 US NAI

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150 63107,242

151 1998-11-05

152 USSR 25,985

153 1999-10-04

121 Disease Resistance Factors

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312* DNA
313* Zea mays

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222 (405)..(406)

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1970-71

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11 12 13 14 15
 Val Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
 1 5 10 15
 Lys Lys Met Val Met Gly Glu Gly Leu Asp Leu Asp Ala Ala Leu Ala
 20 25 30
 Val His Tyr Ala Val Gln His Cys Gly Arg Asp Val Val Lys Ala Leu
 35 40 45
 Ile Gln Leu Gly Ala Ala Asp Val Asn Ser Arg

• 211.1 3
• 211.1 518
• 211.1 DNA
• 211.1 *Oryza sativa*

119
1.1. unsure
1.2. (424)

Unsure
(488)

1 unsure
2 (509)

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•_11 = 5
•_111 = 642
•_111 = DNA
•_111 = *Triticum aestivum*

1.21 unsure
1.22 2b)

- PT unsure

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1105
221 - unsup
222 - 7408

ANSWER

ANSWER

11111 unsure

111 unsure
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unsure 15.65

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• 221 • unsure
• 222 • (585)

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2.1. unsure
2.2. (609), (610)

111 unsure

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123 unsure
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Gln Glu Glu Ser Asp Lys Asp Naa Met Cys Ile Asp Ile Leu Glu

Arg Glu Lys Met Arg Asp Phe Met Thr Ala Glu Asp Ser Val Thr Ser
35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50

Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Ser Tyr Leu Glu Asn
 35 40 45

Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu
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2107 7
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2121 DNA
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 Pro Val His Glu Lys Arg Val Arg Arg Ile His Arg Ala Leu Asp Ser
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Leu Asp Arg Ala Asp Val Ser Tyr Asp Val Ser Tyr Val Asp Phe Asp Ile
 Lys Val Val Ser Ser Ile Leu Leu Asp Leu Ala Met Ala Asp Leu Asp Leu
 Lys Asp Ser Asp Ile Val Tyr Val Ala Leu His Leu Ala Ala Met Asp Arg
 65
 Glu Pro Ala Ile Ile Met Cys Leu Leu Asp Lys Gly Ala Asp Val Ser
 68
 Glu Leu Thr Ala Asp Gly Arg Ser Ala Ile Gly Ile Cys Arg Arg Leu
 111
 Thr Arg Ala Lys Asp Tyr Asp Thr Lys Met Glu Glu Glu Glu Ser
 115
 Asn Lys Asp Arg Leu Cys Ile Asp Ile Leu Glu Arg Glu Met Met Arg
 130
 Asn Pro Met Ala Val Glu Asp Ala Val Thr Ser Pro Leu Leu Ala Asp
 145
 Asp Leu His Met Lys Leu Leu Tyr Leu Glu Asn Arg Val Ala Phe Ala
 161
 Arg Leu Phe Phe Pro Ala Glu Ala Lys Val Ala Met Glu Ile Ala Gln
 180
 Ala Asp Thr Thr Glu Glu Phe Gly Gly Ile Val Ala Val Ala Ala Ser
 195
 Thr Ser Gly Leu Arg Glu Val Asp Leu Asn Glu Thr Pro Val Thr
 210
 Gln Asn Lys Arg Leu Arg Ser Arg Val Asp Ala Leu Met Lys Thr Val
 225
 Glu Leu Gly Arg Arg Tyr Phe Pro Asn Cys Ser Gin Val Leu Asp Lys
 245
 Phe Leu Glu Asp Leu Phe Val Gly Leu Asp Gin Val Tyr Leu Glu
 260
 Arg Gly Thr Ala Asp Glu Gin Lys Val Lys Arg Met Arg Phe Cys Glu
 275
 Leu Lys Glu Asp Val Leu Lys Ala Phe Ser Lys Asp Lys Ala Glu Gly
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 Ser Val Phe Ser Gly Leu Ser Ser Ser Ser Ser Cys Ser Pro Pro Glu
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 Lys Tyr Ala Glu Arg
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Met Glu Pro Pro Ile His Val Thr Asn Ala Phe Ser Asp Ser Asp
1 10 15
Ser Ala Ser Val Glu Glu Gly Gly Ala Asp Ala Asp Ala Asp Val Glu
20 35 50
Ala Leu Arg Arg Leu Ser Asp Asn Leu Ala Ala Ala Phe Arg Ser Pro
35 40 45
Glu Asp Ile Ala Ile Asp Arg Ala Asp Ile Ala Val Pro Gly Gly

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Gly Gly Gly Gly Gly Arg Leu Val His Arg Phe Val Leu Ser Ala
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Arg Ser Phe Leu Val Arg Ala Arg Arg Ala Ala Ala Ala
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Ala Gly Gly Gly Gly Gly Val Val Val Gly Tyr Glu Ala Leu
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Leu Leu Gly Gly Gly Gly Gly Val Glu Val Gly Tyr Glu Ala Leu
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Arg Leu Val Leu Asp Tyr Leu Tyr Ser Gly Arg Val Gly Asp Leu Pro
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Lys Ala Ala Cys Leu Cys Val Asp Glu Asp Cys Ala His Val Gly Cys
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His Pro Ala Val Ala Phe Met Ala Gin Val Leu Phe Ala Ala Ser Thr
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Phe Gln Val Ala Glu Leu Thr Asn Leu Phe Gln Arg Arg Leu Leu Asp
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Val Leu Asp Lys Val Glu Val Asp Asn Leu Ile Leu Ile Leu Ser Val
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Ala Asn Leu Cys Asn Lys Ser Cys Met Lys Leu Leu Glu Arg Cys Leu
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Asp Met Val Val Arg Ser Asn Leu Asp Met Val Thr Leu Glu Lys Ser
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Leu Pro Pro Asp Val Ile Lys Gin Ile Ile Asp Ala Arg Leu Ser Leu
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Gly Leu Ile Ser Pro Glu Asn Lys Gly Phe Pro Asn Lys His Val Arg
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Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Arg Met
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Leu Leu Thr Glu Gly Gin Tyr Asn Ile Asp Asp Ala Phe Ala Leu His
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Tyr Ala Val Glu His Cys Asp Ser Lys Ile Thr Thr Glu Leu Leu Asp
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Leu Ala Leu Ala Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val
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Leu His Ile Ala Ala Arg Arg Glu Pro Lys Ile Ile Val Ser Leu
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Leu Thr Lys Gly Ala Arg Pro Ala Asp Val Thr Phe Asp Gly Arg Lys
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Ala Val Glu Ile Thr Gly Arg Leu Thr Leu Glu Asp Tyr Phe Gly
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Val Thr Gln Glu Gly Lys Phe Thr Cys Ile Lys Asp Arg Ile Cys Ile Glu
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 Ile Lys Glu Glu Ser Ala Glu Arg Arg Asp Pro Glu Leu Gly Glu Ala Ser
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 Ile Lys Glu Glu Ser Ala Glu Arg Arg Asp Pro Glu Leu Gly Glu Ala Ser
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 Val Ser Leu Ala Met Ala Gly Glu Ser Leu Arg Arg Asp Leu Leu Tyr
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 Leu Glu Asn Arg Val Ala Leu Ala Arg Ile Met Phe Pro Met Glu Ala
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 Arg Val Ala Met Asp Ile Ala Glu Val Asp Gly Thr Leu Glu Phe Asn
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 Leu Gly Ser Gly Ala Asn Pro Pro Pro Glu Arg Glu Arg Thr Thr Val
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 Asp Leu Asn Glu Ser Pro Phe Ile Met Lys Glu Glu His Leu Ala Arg
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 Met Thr Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro
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 Arg Cys Ser Asn Val Leu Asp Lys Ile Met Asp Asp Glu Thr Asp Pro
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 Val Ser Leu Gly Arg Asp Thr Ser Ala Glu Lys Arg Lys Arg Phe His
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 Asp Leu Glu Asp Val Leu Glu Lys Ala Phe His Glu Asp Lys Glu
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211 > 2069

11. DNA

• 113: *Oryza sativa*

224

· 22 · unsafe

1993-1994

2400 - 22

1200: 12

210 44

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5213. *Cryza sativa*

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Asp Ala Phe Leu Ser Leu Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg
 1 5 10 15

Pro Ala Pro Asp Asp Val Val Ser Cys Ala Asp Pro Met Cys Pro His
25 30

Asp Ser Cys Pro Pro Ala Ile Arg Phe Asn Val Glu Gln Met Tyr Ala
 35 40 45

Ala Trp Ala Phe Lys Ile Thr Glu Leu Ile Ser Leu Phe Gln Arg Arg
50 55 60

Ile Leu Asn Pro Val Asp Lys Thr Leu Val Glu Asp Val Leu Pro Ile
70 75 80

Leu Ala Val Ala Phe His Ser Ile Leu Thr Pro Val Leu Glu Lys Cys

Ile Ala Arg Ile Ala Arg Ser Asn Leu Asp Asn Val Ser Leu Asp Ly
 100 105 110

Glu Leu Pro Pro Glu Val Ala Val Glu Ile Lys Glu Ile Arg Gin LY

... Ser Gln Pro Asp Glu Gly Asp Thr Val Ile Ser Asp Pro Val His Gl

...Ser Asp Asp Ser Asp Asp Val Glu

Leu Val Lys Ser Leu 184: Arg Lys Lys Ser Pro Ile Thr Ile Asp Asp Ala
 185
 Asn Ala Leu His Tyr Ala Ala Ala 191: Lys Asp Ser Lys Val Val Ser
 192
 Glu Leu Leu Asp Leu Arg Leu Ala Asn Leu Asn Leu Lys Asn Ser Arg
 193
 Ile 200
 Gly Tyr Thr Ala Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile
 201
 Ile Met Cys Leu Leu Asn Lys Phe 211: Ala Val Ser Gln Leu Thr Ala
 225 235
 Asp Gly Gln Ser Ala Met Ser Ile Cys Arg Arg Leu Thr Arg Met Lys
 245 250
 Asp Tyr Asn Thr Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg
 260 265
 Leu Cys Ile Asp Ile Leu Asp Arg Glu Met Ile Arg Lys Pro Met Ala
 275 280
 Val Glu Asp Ser Val Thr Ser Phe Leu Leu Ala Asp Asp Leu His Met
 290 295
 Lys Leu Leu Tyr Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe
 305 310 315
 Pro Ala Glu Ala Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr
 325 330
 Pro GLU Phe Gly Ile Val Pro Ala Ala Ser Thr Ser Gly Lys Leu Lys
 340 345 350
 Glu Val Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg
 355 360 365
 Ser Arg Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr
 370 375
 Phe Pro Asn Cys Ser Gin Val Leu Asp Lys The Leu Glu Asp Asp Ile
 385 390
 Pro Asp Ser Pro Asp Ala Leu Asp Leu Gln Asn Gly Thr Ser Asp Glu
 405 410
 Gin Asn Val Lys Arg Met Asp Phe Iys 421: Leu Iys Gln Asp Val Ile
 420
 Lys Ala Phe Ser Lys Asp Arg Ala Asp Asn Ser Met Phe Ser Ile Leu
 435
 Ser Ser Ser Ser Ser Ser
 440 445

— 1 — 1925

2000 13

280 *W. B. R. HOGG*

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2212. *Eri*
2213. *Tritium aestivum*

5400 · 14

Gly Gln Gly Gln Glu Ser Asn Lys Asp Arg Met Cys Ile Asp Ile Ieu

Figure 1. The effect of the number of nodes on the performance of the proposed algorithm.

Glu Arg Glu Met Met Arg Asn Pro Met Thr Ala Glu Asp Ser Val Thr
20 25 30

Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Ser Tyr Leu Glu
35 40 45

Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala Lys Val
50 55 60

Ala Met Gln Ile Ala Gln Ala Asp Val Thr Pro Glu Val Gly Gly Phe
55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

ser Ala Ala Ser Thr Ser Gly Ile Leu Arg Gln Val Asp Leu Asn Glu

Thr Pro Val Thr Iys Asn Lys Arg Leu Arg Ser Arg Val Asp Ala Le
10 110

Ala Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro Asn Cys Ser Glu
 115 120 125

Val Leu Asp Lys Phe Leu Glu Asp Gly Leu Pro Asp Gly Leu Asp Al
 132 133 134 135 136 137 138 139 140

Arg Pro Tyr Glu Val Lys Glu Asp Val Arg Lys Ala Tyr Ser Lys Asp

Thr-Ala-Asp-Asn-Gly-Met-Pro-Ser-Ala-Leu-Ser-Ser-Asn-Ser-Ser-Ser-Ser

100

210-10
211-10
212-10
213-10
214-10

mitochondria containing membrane proteins. The protein was purified from rat liver mitochondria.

<211> 10

<211> 130

<212> PRT

<213> GlyAsp GlnIle

<401> 10
Met Ile Ala Asp Ser Ala Val Val Val Ile Ala Met Glu Pro Ser Ser

10 10
Met Ile Ala Asp Ser Ala Val Val Val Ile Ala Met Glu Pro Ser Ser

10 10
Ser Ile Thr Ile Ala Ser Ser Ser Ile Tyr Leu Ser Asn Gly Ser Ser

20 20
Ser Ile Thr Ile Ala Ser Ser Ser Ile Tyr Leu Ser Asn Gly Ser Ser

20 20
Pro Cys Ser Val Ser Leu Ala Pro Pro Gly Ala Gly Val Ala Ala

30 40
35 45

Gln Ala Ala Pro Val Ala Ala Gly Glu Gly Gly Gly Gly Gly Gly

50 60
55 65

Gly Gly Gly Gly Ser Ser Ser Val Glu Val Val Ser Leu Asn Arg

65 75 80
65 75 80

Leu Ser Ala Asn Leu Ala Arg Leu Leu Leu Asp Ser Asp Leu Asp Cys

55 65 75
55 65 75

Ser Asp Ala Asp Val Asp Val Ala Asp Gly Gly Pro Pro Val Pro Val

100 105 110
100 105 110

His Arg Cys Ile Leu Ala Ala Arg Ser Thr Phe Phe Tyr Asn Leu Phe

115 120 125
115 120 125

Ala Ala Arg Gly Arg Gly Asp Gly Ala Ala Gly Gly Gly Gly

130 140
130 140

Gly Gly Gly Gly Gly Glu Arg Thr Gly Gly Arg Pro Arg Tyr Lys

145 150 160
145 150 160

Met Glu Glu Leu Val Pro Gly Gly Arg Val Gly Arg Asp Ala Phe Leu

165 170 175
165 170 175

Ser Leu Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Asp

180 185 190
180 185 190

Asp Val Val Ser Cys Ala Asp Pro Met Cys Pro His Asp Ser Cys Pro

195 200 205
195 200 205

Pro Ala Ile Arg Phe Asn Val Glu Gln Met Tyr Ala Ala Trp Ala Phe

210 215 220
210 215 220

Lys Ile Thr Glu Leu Ile Ser Leu Phe Glu Arg Arg Leu Leu Asn Phe

225 230 240
225 230 240

Val Asp Lys Thr Leu Val Glu Asp Val Leu Pro Ile Leu Gln Val Ala

245 250 255
245 250 255

Gln His Ser Glu Leu Thr Pro Val Leu Glu Lys Cys Ile Arg Arg Ile

260 265 270
260 265 270

Ala Asp Ser Asn Leu Asp Asn Val Ser Ile Asp Lys Glu Leu Pro His
 310
 Glu Val Ala Val Glu Ile Lys Glu Ile Arg Glu Lys Ser Ser Pro Asp
 315
 Glu Ser Asp Thr Val Val Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
 320
 325
 Glu Ser Asp Ile Val Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
 325
 330
 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
 335
 340
 Leu Leu Asn Glu Ser Glu Ile Thr Leu Asp Asp Ala Asn Ala Leu His
 345
 350
 Tyr Ala Ala Ala Tyr Cys Asp Ser Lys Val Val Ser Glu Leu Leu Asp
 355
 360
 Leu Arg Leu Ala Asn Leu Asn Ser Arg Gly Tyr Thr Ala
 370
 375
 Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
 380
 385
 Leu Asn Lys Gly Ala Ala Val Ser Glu Leu Thr Ala Asp Gly Glu Ser
 390
 395
 Ala Met Ser Ile Cys Arg Arg Leu Thr Arg Met Lys Asp Tyr Asn Thr
 400
 405
 Lys Met Glu Glu Gly Glu Ser Asn Ile Asp Arg Asn Leu Cys Ile Asp
 410
 415
 Ile Leu Asp Arg Glu Met Ile Arg Lys Pro Met Ala Val Glu Asp Ser
 420
 425
 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
 430
 435
 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
 440
 445
 Lys Val Ala Met Glu Ile Ala Ile Asp Thr Ile Asp Glu Phe Gly
 450
 455
 Ile Val Pro Ala Ala Ser Thr Ser Gly Lys Leu Lys Glu Val Asp Leu
 460
 465
 Asn Glu Thr Pro Val Thr Glu Asn Lys Arg Leu Arg Ser Arg Val Asp
 470
 475
 Ala Leu Met Lys Thr Val Glu Leu Phe Arg Arg Ile Phe Pro Asp Cys
 480
 485
 Ser Glu Val Leu Asp Lys Phe Leu Ile Asp Asp Leu Pro Asp Ser Pro
 490
 495
 Asp Ala Leu Asp Leu Val Asn Phe Thr Leu Asp Glu Glu Asn Val Lys
 500
 505

Ala Met Arg Ile Lys Glu Ile Lys Ala Asp Val Arg Asp Ile Asp Lys Ala Phe Ser
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 329 330 331 332 333 334 335 336 337 338 339 339 340 341 342 343 344 345 346 347 348 349 349 350 351 352 353 354 355 356 357 358 359 359 360 361 362 363 364 365 366 367 368 369 369 370 371 372 373 374 375 376 377 378 379 379 380 381 382 383 384 385 386 387 388 389 389 390 391 392 393 394 395 396 397 398 399 399 400 401 402 403 404 405 406 407 408 409 409 410 411 412 413 414 415 416 417 418 419 419 420 421 422 423 424 425 426 427 428 429 429 430 431 432 433 434 435 436 437 438 439 439 440 441 442 443 444 445 446 447 448 449 449 450 451 452 453 454 455 456 457 458 459 459 460 461 462 463 464 465 466 467 468 469 469 470 471 472 473 474 475 476 477 478 479 479 480 481 482 483 484 485 486 487 488 489 489 490 491 492 493 494 495 496 497 498 499 499 500 501 502 503 504 505 506 507 508 509 509 510 511 512 513 514 515 516 517 518 519 519 520 521 522 523 524 525 526 527 528 529 529 530 531 532 533 534 535 536 537 538 539 539 540 541 542 543 544 545 546 547 548 549 549 550 551 552 553 554 555 556 557 558 559 559 560 561 562 563 564 565 566 567 568 569 569 570 571 572 573 574 575 576 577 578 579 579 580 581 582 583 584 585 586 587 588 589 589 590 591 592 593 594 595 596 597 598 599 599 600 601 602 603 604 605 606 607 608 609 609 610 611 612 613 614 615 616 617 618 619 619 620 621 622 623 624 625 626 627 628 629 629 630 631 632 633 634 635 636 637 638 639 639 640 641 642 643 644 645 646 647 648 649 649 650 651 652 653 654 655 656 657 658 659 659 660 661 662 663 664 665 666 667 668 669 669 670 671 672 673 674 675 676 677 678 679 679 680 681 682 683 684 685 686 687 688 689 689 690 691 692 693 694 695 696 697 698 699 699 700 701 702 703 704 705 706 707 708 709 709 710 711 712 713 714 715 716 717 718 719 719 720 721 722 723 724 725 726 727 728 729 729 730 731 732 733 734 735 736 737 738 739 739 740 741 742 743 744 745 746 747 748 749 749 750 751 752 753 754 755 756 757 758 759 759 760 761 762 763 764 765 766 767 768 769 769 770 771 772 773 774 775 776 777 778 779 779 780 781 782 783 784 785 786 787 788 789 789 790 791 792 793 794 795 796 797 798 799 799 800 801 802 803 804 805 806 807 808 809 809 810 811 812 813 814 815 816 817 818 819 819 820 821 822 823 824 825 826 827 828 829 829 830 831 832 833 834 835 836 837 838 839 839 840 841 842 843 844 845 846 847 848 849 849 850 851 852 853 854 855 856 857 858 859 859 860 861 862 863 864 865 866 867 868 869 869 870 871 872 873 874 875 876 877 878 879 879 880 881 882 883 884 885 886 887 888 889 889 890 891 892 893 894 895 896 897 898 899 899 900 901 902 903 904 905 906 907 908 909 909 910 911 912 913 914 915 916 917 918 919 919 920 921 922 923 924 925 926 927 928 929 929 930 931 932 933 934 935 936 937 938 939 939 940 941 942 943 944 945 946 947 948 949 949 950 951 952 953 954 955 956 957 958 959 959 960 961 962 963 964 965 966 967 968 969 969 970 971 972 973 974 975 976 977 978 979 979 980 981 982 983 984 985 986 987 988 989 989 990 991 992 993 994 995 996 997 998 999 999 1000

Leu Ile Pro Val Ile Val Lys Cys Ile Ile Asp Arg Arg Lys Ala Leu
 385
 Gly Ile Ser Thr Val Pro Ile Lys Val Lys His Val Ser Asn Val His Lys
 390
 Ala Ile Asp Thr Asn Asp Ile Cys Ile Val Lys Ile Leu Leu Lys Glu
 395
 Asp His Thr Asn Leu Asp Asp Ala Phe Ala Leu His Phe Ala Val Ala
 400
 Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala
 395
 300
 Asp Val Asn His Arg Asn Pro Asp Gly Tyr Thr Val Leu His Val Ala
 325
 330
 335
 Ala Met Arg Lys Glu Pro Glu Ile Leu Ser Leu Leu Glu Lys Gly
 340
 345
 350
 Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile
 355
 360
 365
 Ala Lys Glu Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Glu
 370
 375
 380
 Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln
 385
 390
 400
 Glu Asp Lys Arg Cys Cys Ile Pro Asp Asp Val Pro Pro Ser Phe Ala
 405
 410
 415
 Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg
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 425
 430
 Val Ala Leu Ala Cln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met
 435
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 445
 Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu
 450
 455
 460
 Glu Pro Asp Arg Leu Thr Gly Thr Ivs Arg Thr Ser Phe Val Lys
 465
 470
 475
 480
 Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala
 485
 490
 495
 Ile Ser Lys Thr Val Glu Leu Cys Arg Phe Phe Pro Arg Lys Ser
 500
 505
 510
 Ala Val Leu Asp Glu Ile Met Asn Lys Glu Asp Leu Thr Cln Leu Ala
 515
 520
 525
 Cys Gly Glu Asp Asp Thr Ala Gln Lys Arg Leu Glu Lys Lys Glu Arg
 530
 535
 Tyr Met Asp Ile Glu Ile Thr Ile Lys Lys Ala Thr Ser Glu Asp Asn
 540
 545

Leu His Leu . Glu Asn Ser Val Leu Leu Arg Ser Thr Ser Ser Thr Ser
Arg
Lys Ser Thr Arg Arg Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg
Arg
Arg